BLAST Basic Local Alignment Search Tool

Job Title: Nucleotide sequence (64 letters)

-

BLASTN 2.2.18 (Mar-02-2008)

Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped
BLAST and PSI-BLAST: a new generation of protein database search programs",
Nucleic Acids Res. 25:3389-3402. RID: 1HASZE0V012 Database: human build 36.3
reference assembly genomic scaffolds 49,942 sequences; 5,818,011,736 total
letters

| Genome View | Show positions of the BLAST hits in the human genome using the Entrez Genomes MapViewer |

Query= Length=64

Distribution of 22 Blast Hits on the Query Sequence
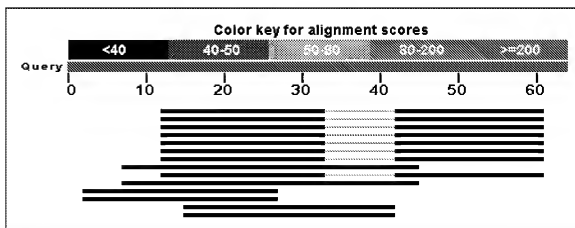
Distance tree of results NEW

Legend for links to other resources: ◻ UniGene ◻ GEO G Gene ◻ Structure ◻

Sequences producing significant alignments:
(Click headers to sort columns)

Transcripts

NM_001080125.1	Homo sapiens caspase 8, apoptosis-related cysteine peptidase (CASP8), transcript variant G, mRNA	39.2	74.7	62%	0.32	100%	U G M
NM_001080124.1	Homo sapiens caspase 8, apoptosis-related cysteine peptidase (CASP8), transcript variant F, mRNA	39.2	74.7	62%	0.32	100%	U G M
NM_033358.3	Homo sapiens caspase 8, apoptosis-related cysteine peptidase (CASP8), transcript variant E, mRNA	39.2	74.7	62%	0.32	100%	U E G M
NM_033356.3	Homo sapiens caspase 8, apoptosis-related cysteine peptidase (CASP8), transcript variant C, mRNA	39.2	74.7	62%	0.32	100%	U E G M
NM_001228.4	Homo sapiens caspase 8, apoptosis-related cysteine peptidase (CASP8), transcript variant A, mRNA	39.2	74.7	62%	0.32	100%	U E G M
NM_033355.3	Homo sapiens caspase 8, apoptosis-related cysteine peptidase (CASP8), transcript variant B, mRNA	39.2	74.7	62%	0.32	100%	U E G M

Genomic sequences [show first]

NW_001838863.1	Homo sapiens chromosome 2 genomic contig, alternate assembly (based on HuRef SCAF_1103279188396)	39.2	74.7	62%	0.32	100%
NW_001839136.1	Homo sapiens chromosome 8 genomic contig, alternate assembly (based on HuRef SCAF_1103279188253)	39.2	39.2	59%	0.32	84%
NT_005403.16	Homo sapiens chromosome 2 genomic contig, reference assembly	39.2	74.7	62%	0.32	100%
NT_008046.15	Homo sapiens chromosome 8 genomic contig, reference assembly	39.2	39.2	59%	0.32	84%
NW_001838084.2	Homo sapiens chromosome 13 genomic contig, alternate assembly (based on HuRef SCAF_1103279188152)	37.4	37.4	39%	1.1	92%
NT_009952.14	Homo sapiens chromosome 13 genomic contig, reference assembly	37.4	37.4	39%	1.1	92%
NW_001842360.1	Homo sapiens chromosome X genomic contig, alternate assembly (based on HuRef SCAF_1103279188416)	35.6	35.6	42%	3.9	88%
NT_011757.15	Homo sapiens chromosome X genomic contig, reference assembly	35.6	35.6	42%	3.9	88%

Alignments

>ref|NM_001080125.1| `UGM` Homo sapiens caspase 8, apoptosis-related cysteine pe
(CASP8), transcript variant G, mRNA
Length=2938

 GENE ID: 841 CASP8 | caspase 8, apoptosis-related cysteine peptidase
[Homo sapiens] (Over 100 PubMed links)

                                              Sort alignments for this
                                                E value Score Percen
                                                Query start position

 Score = 39.2 bits (42), Expect = 0.32
 Identities = 21/21 (100%), Gaps = 0/21 (0%)
 Strand=Plus/Plus

Query 13   AAGTTCCTGAGCCTGGACTAC 33
            |||||||||||||||||||||
Sbjct 445 AAGTTCCTGAGCCTGGACTAC 465

 Score = 35.6 bits (38), Expect = 3.9
 Identities = 19/19 (100%), Gaps = 0/19 (0%)
 Strand=Plus/Minus

Query 43   GTAGTCCAGGCTCAGGAAC 61
            |||||||||||||||||||
Sbjct 465 GTAGTCCAGGCTCAGGAAC 447

>ref|NM_001080124.1| `UGM` Homo sapiens caspase 8, apoptosis-related cysteine pe
(CASP8), transcript variant F, mRNA
Length=2750

 GENE ID: 841 CASP8 | caspase 8, apoptosis-related cysteine peptidase
[Homo sapiens] (Over 100 PubMed links)

                                              Sort alignments for this
                                                E value Score Percen
                                                Query start position

 Score = 39.2 bits (42), Expect = 0.32
 Identities = 21/21 (100%), Gaps = 0/21 (0%)
 Strand=Plus/Plus

Query 13   AAGTTCCTGAGCCTGGACTAC 33
            |||||||||||||||||||||
Sbjct 302 AAGTTCCTGAGCCTGGACTAC 322

 Score = 35.6 bits (38), Expect = 3.9
 Identities = 19/19 (100%), Gaps = 0/19 (0%)
 Strand=Plus/Minus

Query 43   GTAGTCCAGGCTCAGGAAC 61
            |||||||||||||||||||
Sbjct 322 GTAGTCCAGGCTCAGGAAC 304

>ref|NM_033358.3| `UGM` Homo sapiens caspase 8, apoptosis-related cysteine pep
(CASP8), transcript variant E, mRNA
Length=1123

GENE ID: 841 CASP8 | caspase 8, apoptosis-related cysteine peptidase
[Homo sapiens] (Over 100 PubMed links)

Score = 39.2 bits (42), Expect = 0.32
Identities = 21/21 (100%), Gaps = 0/21 (0%)
Strand=Plus/Plus

```
Query   13    AAGTTCCTGAGCCTGGACTAC    33
              |||||||||||||||||||||
Sbjct   370   AAGTTCCTGAGCCTGGACTAC    390
```

Score = 35.6 bits (38), Expect = 3.9
Identities = 19/19 (100%), Gaps = 0/19 (0%)
Strand=Plus/Minus

```
Query   43    GTAGTCCAGGCTCAGGAAC    61
              |||||||||||||||||||
Sbjct   390   GTAGTCCAGGCTCAGGAAC    372
```

>ref|NM_033356.3| █UESGM Homo sapiens caspase 8, apoptosis-related cysteine pep
(CASP8), transcript variant C, mRNA
Length=2655

GENE ID: 841 CASP8 | caspase 8, apoptosis-related cysteine peptidase
[Homo sapiens] (Over 100 PubMed links)

Score = 39.2 bits (42), Expect = 0.32
Identities = 21/21 (100%), Gaps = 0/21 (0%)
Strand=Plus/Plus

```
Query   13    AAGTTCCTGAGCCTGGACTAC    33
              |||||||||||||||||||||
Sbjct   207   AAGTTCCTGAGCCTGGACTAC    227
```

Score = 35.6 bits (38), Expect = 3.9
Identities = 19/19 (100%), Gaps = 0/19 (0%)
Strand=Plus/Minus

```
Query   43    GTAGTCCAGGCTCAGGAAC    61
              |||||||||||||||||||
Sbjct   227   GTAGTCCAGGCTCAGGAAC    209
```

>ref|NM_001228.4| █UESGM Homo sapiens caspase 8, apoptosis-related cysteine pep
(CASP8), transcript variant A, mRNA
Length=2914

GENE ID: 841 CASP8 | caspase 8, apoptosis-related cysteine peptidase
[Homo sapiens] (Over 100 PubMed links)

Score = 39.2 bits (42), Expect = 0.32
Identities = 21/21 (100%), Gaps = 0/21 (0%)
Strand=Plus/Plus

```
Query  13   AAGTTCCTGAGCCTGGACTAC   33
            |||||||||||||||||||||
Sbjct  370  AAGTTCCTGAGCCTGGACTAC   390


 Score = 35.6 bits (38),  Expect = 3.9
 Identities = 19/19 (100%), Gaps = 0/19 (0%)
 Strand=Plus/Minus

Query  43   GTAGTCCAGGCTCAGGAAC   61
            |||||||||||||||||||
Sbjct  390  GTAGTCCAGGCTCAGGAAC   372
```

>ref|NM_033355.3| U R G N Homo sapiens caspase 8, apoptosis-related cysteine pep
(CASP8), transcript variant B, mRNA
Length=2769

 GENE ID: 841 CASP8 | caspase 8, apoptosis-related cysteine peptidase
[Homo sapiens] (Over 100 PubMed links)

                                          Sort alignments for this
                                          E value Score Percen
                                          Query start position

 Score = 39.2 bits (42), Expect = 0.32
 Identities = 21/21 (100%), Gaps = 0/21 (0%)
 Strand=Plus/Plus

```
Query  13   AAGTTCCTGAGCCTGGACTAC   33
            |||||||||||||||||||||
Sbjct  276  AAGTTCCTGAGCCTGGACTAC   296


 Score = 35.6 bits (38),  Expect = 3.9
 Identities = 19/19 (100%), Gaps = 0/19 (0%)
 Strand=Plus/Minus

Query  43   GTAGTCCAGGCTCAGGAAC   61
            |||||||||||||||||||
Sbjct  296  GTAGTCCAGGCTCAGGAAC   278
```

>ref|NM_001838863.1|Hs2_WGA256_36 [image] Homo sapiens chromosome 2 genomic contig, al
(based on HuRef SCAF_1103279188396)
Length=44081246

                                          Sort alignments for this
                                          E value Score Percen
                                          Query start position

 Features in this part of subject sequence:
   caspase 8 isoform G precursor
   caspase 8 isoform E

 Score = 39.2 bits (42), Expect = 0.32
 Identities = 21/21 (100%), Gaps = 0/21 (0%)
 Strand=Plus/Plus

```
Query  13        AAGTTCCTGAGCCTGGACTAC   33
                 |||||||||||||||||||||
Sbjct  27538620  AAGTTCCTGAGCCTGGACTAC   27538640
```

 Features in this part of subject sequence:
   caspase 8 isoform G precursor
   caspase 8 isoform E

```
  Score = 35.6 bits (38),  Expect = 3.9
  Identities = 19/19 (100%), Gaps = 0/19 (0%)
  Strand=Plus/Minus

Query  43         GTAGTCCAGGCTCAGGAAC  61
                  |||||||||||||||||||
Sbjct  27538640   GTAGTCCAGGCTCAGGAAC  27538622
```

>ref|NW_001839136.1|Hs8_WGA529_36 🔲 Homo sapiens chromosome 8 genomic contig, al
(based on HuRef SCAF_1103279188253)
Length=44702525

  Features in this part of subject sequence:
    hypothetical protein

```
  Score = 39.2 bits (42),  Expect = 0.32
  Identities = 32/38 (84%), Gaps = 1/38 (2%)
  Strand=Plus/Plus

Query  8          CCAAAAAGTTCCTGAGCCTGGACTACTCTCTTGAAGTA  45
                  ||| ||||||| ||||||||||| |||||||| | ||||
Sbjct  22623652   CCATAAAGTTACTGAGCCTGGA-TACTCCTAAATTA   22623688
```

>ref|NT_005403.16|Hs2_5560 🔲 Homo sapiens chromosome 2 genomic contig, reference
Length=84213157

                                              Sort alignments for this
                                                E value Score Percen
                                                Query start position

  Features in this part of subject sequence:
    caspase 8 isoform G precursor
    caspase 8 isoform E

```
  Score = 39.2 bits (42),  Expect = 0.32
  Identities = 21/21 (100%), Gaps = 0/21 (0%)
  Strand=Plus/Plus

Query  13         AAGTTCCTGAGCCTGGACTAC  33
                  |||||||||||||||||||||
Sbjct  52340693   AAGTTCCTGAGCCTGGACTAC  52340713
```

  Features in this part of subject sequence:
    caspase 8 isoform G precursor
    caspase 8 isoform E

```
  Score = 35.6 bits (38),  Expect = 3.9
  Identities = 19/19 (100%), Gaps = 0/19 (0%)
  Strand=Plus/Minus

Query  43         GTAGTCCAGGCTCAGGAAC  61
                  |||||||||||||||||||
Sbjct  52340713   GTAGTCCAGGCTCAGGAAC  52340695
```

>ref|NT_008046.15|Hs8_8203 🔲 Homo sapiens chromosome 8 genomic contig, reference
Length=57155273

  Features in this part of subject sequence:
    hypothetical protein

```
  Score = 39.2 bits (42),  Expect = 0.32
  Identities = 32/38 (84%), Gaps = 1/38 (2%)
  Strand=Plus/Plus

Query  8          CCAAAAAGTTCCTGAGCCTGGACTACTCTCTTGAAGTA  45
```

```
                ||| |||||| ||||||||||| ||||||| | || ||
Sbjct  22578869  CCATAAAGTTACTGAGCCTGGA-TACTCTCCTAAATTA  22578905


>ref|NW_001838084.2|Hs13_WGA793_36 🔲 Homo sapiens chromosome 13 genomic contig,
(based on HuRef SCAF_1103279188152)
Length=25468656

 Features flanking this part of subject sequence:
   377332 bp at 5' side: hypothetical protein LOC728215
   129111 bp at 3' side: similar to hCG1639781


 Score = 37.4 bits (40),  Expect = 1.1
 Identities = 23/25 (92%), Gaps = 0/25 (0%)
 Strand=Plus/Plus

Query  3          CTTTTCCAAAAAGTTCCTGAGCCTG  27
                  |||| ||||| |||||||||||||
Sbjct  4921049    CTTTACCAAATAGTTCCTGAGCCTG  4921073


>ref|NT_009952.14|Hs13_10109 🔲 Homo sapiens chromosome 13 genomic contig, refere
Length=25443670

 Features flanking this part of subject sequence:
   225344 bp at 5' side: arginine and glutamate rich 1
   377210 bp at 3' side: hypothetical protein LOC728215


 Score = 37.4 bits (40),  Expect = 1.1
 Identities = 23/25 (92%), Gaps = 0/25 (0%)
 Strand=Plus/Minus

Query  3          CTTTTCCAAAAAGTTCCTGAGCCTG  27
                  |||| ||||| |||||||||||||
Sbjct  20535311   CTTTACCAAATAGTTCCTGAGCCTG  20535287


>ref|NW_001842360.1|HsX_WGA1321_36 🔲 Homo sapiens chromosome X genomic contig, a
(based on HuRef SCAF_1103279188416)
Length=28681338

 Features in this part of subject sequence:
   protein phosphatase with EF hand calcium-binding domain 1...
   protein phosphatase with EF hand calcium-binding domain 1...


 Score = 35.6 bits (38),  Expect = 3.9
 Identities = 24/27 (88%), Gaps = 0/27 (0%)
 Strand=Plus/Minus

Query  16         TTCCTGAGCCTGGACTACTCTCTTGAA  42
                  ||||||||||||| || ||||| |||
Sbjct  10286062   TTCCTGAGCCTGGAATAGTCTCTGGAA  10286036


>ref|NT_011757.15|HsX_11914 🔲 Homo sapiens chromosome X genomic contig, referenc
Length=34879939

 Features in this part of subject sequence:
   protein phosphatase with EF hand calcium-binding domain 1...
   protein phosphatase with EF hand calcium-binding domain 1...


 Score = 35.6 bits (38),  Expect = 3.9
 Identities = 24/27 (88%), Gaps = 0/27 (0%)
 Strand=Plus/Minus

Query  16         TTCCTGAGCCTGGACTACTCTCTTGAA  42
                  ||||||||||||| || ||||| |||
Sbjct  16522474   TTCCTGAGCCTGGAATAGTCTCTGGAA  16522448
```

```
   Database: human build 36.3 reference assembly genomic scaffolds
     Posted date:  Apr 16, 2008  7:40 PM
   Number of letters in database: 1,523,044,440
   Number of sequences in database:  49,942

Lambda      K        H
   0.634     0.408     0.912
Gapped
Lambda      K        H
   0.634     0.408     0.912
Matrix: blastn matrix:2 -3
Gap Penalties: Existence: 5, Extension: 2
Number of Sequences: 49942
Number of Hits to DB: 437151
Number of extensions: 24062
Number of successful extensions: 152
Number of sequences better than 10: 0
Number of HSP's better than 10 without gapping: 0
Number of HSP's gapped: 152
Number of HSP's successfully gapped: 0
Length of query: 64
Length of database: 5818011736
Length adjustment: 30
Effective length of query: 34
Effective length of database: 5816513476
Effective search space: 197761458184
Effective search space used: 197761458184
A: 0
X1: 22 (20.1 bits)
X2: 33 (29.8 bits)
X3: 110 (99.2 bits)
S1: 30 (28.3 bits)
S2: 37 (34.6 bits)
```